



PCT

RAW SEQUENCE LISTING DATE: 12/10/2004
PATENT APPLICATION: US/10/516,505 TIME: 14:21:08

Input Set : A:\PTS-0055WO.txt
Output Set: N:\CRF4\12102004\J516505.raw

**Does Not Comply
Corrected Diskette Needed**

P. b

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DATE: 12/10/2004
TIME: 14:21:08

Input Set : A:\PTS-0055WO.txt
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67 <221> NAME/KEY: CDS		
68 <222> LOCATION: (34) . . . (1137)		
70 <400> SEQUENCE: 4		
71 ggctctgcgg ggtggcagc tcccgccct gcc atg agc tct ccg ccg ccc acc	54	
72 Met Ser Ser Pro Pro Pro Thr		
73 1 5		
75 cgc agt ggc ttt tac cgc cag gag gtg acc aag acg gcc tgg gag gtg	102	
76 Arg Ser Gly Phe Tyr Arg Gln Glu Val Thr Lys Thr Ala Trp Glu Val		
77 10 15 20		
79 cgc gcc gtg tac cgg gac ctg cag ccc gtg ggc tcg ggc gcc tac ggc	150	
80 Arg Ala Val Tyr Arg Asp Leu Gln Pro Val Gly Ser Gly Ala Tyr Gly		
81 25 30 35		
83 gcg gtg tgc tcg gcc gtg gac ggc cgc acc ggc gct aag gtt gcc atc	198	
84 Ala Val Cys Ser Ala Val Asp Gly Arg Thr Gly Ala Lys Val Ala Ile		
85 40 45 50 55		
87 aag aag ctg tat cgg ccc ttc cag tcc gag ctg ttc gcc aag ctc gcc	246	
88 Lys Lys Leu Tyr Arg Pro Phe Gln Ser Glu Leu Phe Ala Lys Leu Ala		
89 60 65 70		
91 tac cgc gag ctg cgc ctg ctc aag cac atg cgc cac gag aac gtg atc	294	
92 Tyr Arg Glu Leu Arg Leu Leu Lys His Met Arg His Glu Asn Val Ile		
93 75 80 85		
95 ggg ctg ctg gac gta ttc act cct gat gag acc ctg gat gac ttc acg	342	
96 Gly Leu Leu Asp Val Phe Thr Pro Asp Glu Thr Leu Asp Asp Phe Thr		
97 90 95 100		
99 gac ttt tac ctg gtg atg ccg ttc atg ggc acc gac ctg ggc aag ctc	390	
100 Asp Phe Tyr Leu Val Met Pro Phe Met Gly Thr Asp Leu Gly Lys Leu		
101 105 110 115		
103 atg aaa cat gag aag cta ggc gag gac cgg atc cag ttc ctc gtg tac	438	
104 Met Lys His Glu Lys Leu Gly Glu Asp Arg Ile Gln Phe Leu Val Tyr		
105 120 125 130 135		
107 cag atg atg aag ggg ctg agg tat atc cac gct gcc ggc atc atc cac	486	
108 Gln Met Met Lys Gly Leu Arg Tyr Ile His Ala Ala Gly Ile Ile His		
109 140 145 150		
111 aga gac ctg aag ccc ggc aac ctg gct gtg aac gaa gac tgt gag ctg	534	
112 Arg Asp Leu Lys Pro Gly Asn Leu Ala Val Asn Glu Asp Cys Glu Leu		
113 155 160 165		
115 aag atc ctg gac ttc ggc ctg gcc agg cag gca gac agt gag atg act	582	
116 Lys Ile Leu Asp Phe Gly Leu Ala Arg Gln Ala Asp Ser Glu Met Thr		
117 170 175 180		
119 ggg tac gtg gtg acc cgg tgg tac cgg gct ccc gag gtc atc ttg aat	630	
120 Gly Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Val Ile Leu Asn		
121 185 190 195		
123 tgg atc gcg tac acg cag acg gtg gac atc tgg tct gtg ggc tgc atc	678	
124 Trp Ile Ala Tyr Thr Gln Thr Val Asp Ile Trp Ser Val Gly Cys Ile		
125 200 205 210 215		
127 atg gcg gag atg atc aca ggc aag acg ctg ttc aag ggc agc gac cac	726	
128 Met Ala Glu Met Ile Thr Gly Lys Thr Leu Phe Lys Gly Ser Asp His		
129 220 225 230		
131 ctg gac cag ctg aag gag atc atg aag gtg acg ggg acg cct ccg gct	774	

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132	Leu	Asp	Gln	Leu	Lys	Glu	Ile	Met	Lys	Val	Thr	Gly	Thr	Pro	Pro	Ala	
133				235				240						245			
135	gag	ttt	gtg	cag	cg	ctg	cag	agc	gat	gag	gcc	aag	aac	tac	atg	aag	822
136	Glu	Phe	Val	Gln	Arg	Leu	Gln	Ser	Asp	Glu	Ala	Lys	Asn	Tyr	Met	Lys	
137				250				255				260					
139	ggc	ctc	ccc	gaa	ttg	gag	aag	aag	gat	ttt	gcc	tct	atc	ctg	acc	aat	870
140	Gly	Leu	Pro	Glu	Leu	Glu	Lys	Lys	Asp	Phe	Ala	Ser	Ile	Leu	Thr	Asn	
141				265				270				275					
143	gca	agc	cct	ctg	gct	gtg	aac	ctc	ctg	gag	aag	atg	ctg	gtg	ctg	gac	918
144	Ala	Ser	Pro	Leu	Ala	Val	Asn	Leu	Leu	Glu	Lys	Met	Leu	Val	Leu	Asp	
145				280				285				290			295		
147	gcg	gac	atc	agg	ttg	act	gca	ggc	gag	ttt	ctt	tcc	cat	ccc	tac	ttc	966
148	Ala	Asp	Ile	Arg	Leu	Thr	Ala	Gly	Glu	Phe	Leu	Ser	His	Pro	Tyr	Phe	
149					300				305				310				
151	gag	tcc	ctg	cac	gac	acg	gaa	gat	gag	ccc	cag	gtc	cag	aag	tat	gat	1014
152	Glu	Ser	Leu	His	Asp	Thr	Glu	Asp	Glu	Pro	Gln	Val	Gln	Lys	Tyr	Asp	
153				315				320				325					
155	gac	tcc	ttt	gac	tac	ttt	gac	cg	aca	ctg	gat	gaa	tgg	aag	cgt	gtt	1062
156	Asp	Ser	Phe	Asp	Tyr	Phe	Asp	Arg	Thr	Leu	Asp	Glu	Trp	Lys	Arg	Val	
157				330				335				340					
159	act	tac	aaa	gag	gtg	ctc	agc	tcc	aag	cct	ccc	cg	cag	ctg	ggg	gcc	1110
160	Thr	Tyr	Lys	Glu	Val	Leu	Ser	Phe	Lys	Pro	Pro	Arg	Gln	Leu	Gly	Ala	
161				345				350				355					
163	agg	gtc	tcc	aag	gag	acg	cct	ctg	tga	agatctctgg	gtccgggggt						1157
164	Arg	Val	Ser	Lys	Glu	Thr	Pro	Leu									
165				360				365									
167	ggcagtgagg	accaccca	ccttccac	ccttccac	gagagggac	tctcggtgcc	accttgac										1217
169	tggctgggc	ttgcataccca	aggcatccat	cagagcagac	gcccgggttc	catggacc	c										1277
171	cctcccccact	gccatgcctc	tgctcttgg	cgccatcat	ggaggagac	ctgaactt	c										1337
173	tggacaagac	ctctggccga	cctggggatg	gcctctgate	cctggagcag	tggaaacacaa											1397
175	aaaaacaatac	tctcagaaac	ctcagagctg	gtggggctcc	agatcagcct	tggcctctga											1457
177	gccctgcctg	ctctgggcca	tgcagagggaa	ggacagaggg	tggagcagg	gcaccaactc											1517
179	agggacatcc	cctctcttgg	gcgacgtcag	tggaccttcc	tgcaccccca	gcctggaaatg											1577
181	taaatcagct	gtgtgggcc	cgcgtggctg	gaagaaaata	gaccctttt	tagtccaaa											1637
183	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaa	aaaaaaa	aaaaaaa											1670
186	<210>	SEQ ID NO:	5														
187	<211>	LENGTH:	20														
188	<212>	TYPE:	DNA														
189	<213>	ORGANISM:	Artificial Sequence														
191	<220>	FEATURE:															
193	<223>	OTHER INFORMATION:	PCR Primer														
195	<400>	SEQUENCE:	5														
196	ctcggtgcc	ccttgcac														20	
199	<210>	SEQ ID NO:	6														
200	<211>	LENGTH:	16														
201	<212>	TYPE:	DNA														
202	<213>	ORGANISM:	Artificial Sequence														
204	<220>	FEATURE:															
206	<223>	OTHER INFORMATION:	PCR Primer														

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```

208 <400> SEQUENCE: 6
209 tggaaacccgg gcgtct          16
212 <210> SEQ ID NO: 7
213 <211> LENGTH: 24
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Probe
221 <400> SEQUENCE: 7
222 ttgcattcca aggcatccat caga          24
225 <210> SEQ ID NO: 8
226 <211> LENGTH: 19
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
232 <223> OTHER INFORMATION: PCR Primer
234 <400> SEQUENCE: 8
235 gaaggtaaag gtcggagtc          19
238 <210> SEQ ID NO: 9
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
247 <400> SEQUENCE: 9
248 gaagatggtg atgggatttc          20
251 <210> SEQ ID NO: 10
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
258 <223> OTHER INFORMATION: PCR Probe
260 <400> SEQUENCE: 10
261 caagcttccc gttctcagcc          20
264 <210> SEQ ID NO: 11
265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
271 <223> OTHER INFORMATION: Antisense Oligonucleotide
273 <400> SEQUENCE: 11
274 ccttcatcat ctggcacacg          20
277 <210> SEQ ID NO: 12
278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
284 <223> OTHER INFORMATION: Antisense Oligonucleotide
286 <400> SEQUENCE: 12

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RAW SEQUENCE LISTING
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Input Set : A:\PTS-0055WO.txt
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287 tccttcagct ggtccagggtg 20
290 <210> SEQ ID NO: 13
291 <211> LENGTH: 20
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
297 <223> OTHER INFORMATION: Antisense Oligonucleotide
299 <400> SEQUENCE: 13
300 ccaccagctc tgagggttct 20
303 <210> SEQ ID NO: 14
304 <211> LENGTH: 20
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
310 <223> OTHER INFORMATION: Antisense Oligonucleotide
312 <400> SEQUENCE: 14
313 ggagagctca tggcaggccc 20
316 <210> SEQ ID NO: 15
317 <211> LENGTH: 20
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
323 <223> OTHER INFORMATION: Antisense Oligonucleotide
325 <400> SEQUENCE: 15
326 gtggcgcatg tgcttgagca 20
329 <210> SEQ ID NO: 16
330 <211> LENGTH: 20
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
336 <223> OTHER INFORMATION: Antisense Oligonucleotide
338 <400> SEQUENCE: 16
339 cccttcatca tctggtagac 20
342 <210> SEQ ID NO: 17
343 <211> LENGTH: 20
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
349 <223> OTHER INFORMATION: Antisense Oligonucleotide
351 <400> SEQUENCE: 17
352 atccagggtc tcatacaggag 20
355 <210> SEQ ID NO: 18
356 <211> LENGTH: 20
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence
360 <220> FEATURE:
362 <223> OTHER INFORMATION: Antisense Oligonucleotide
364 <400> SEQUENCE: 18
365 cccggagccc agagatcttc 20

10/5/6, 505

6

??
??
??
??

delete at end of file

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/516,505

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Input Set : A:\PTS-0055WO.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:71; N Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
Seq#:75; N Pos. 727

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8

VERIFICATION SUMMARY
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Input Set : A:\PTS-0055WO.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1007 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1011 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:71
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0
L:1307 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:75,Line#:1305
L:1332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:720
L:3333 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:3335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:233
L:3335 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:3337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:233
L:3337 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:3339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:233
L:3339 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1